

04-10-01

0288

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/802,674

DATE: 03/27/2001
 TIME: 15:29:23

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3 <110> APPLICANT: Macina, Roberto A
 4 Piderit, Alejandra
 5 Sun, Yongming
 7 <120> TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
 8 Treating Gastrointestinal Cancer
 10 <130> FILE REFERENCE: DEX-0142
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/802,674
 C--> 13 <141> CURRENT FILING DATE: 2001-03-09
 15 <150> PRIOR APPLICATION NUMBER: 60/188,061
 16 <151> PRIOR FILING DATE: 2000-03-09
 18 <160> NUMBER OF SEQ ID NOS: 13
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64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapiens
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72 20 25 30
74 Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val
75 35 40 45
77 Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe
78 50 55 60
80 Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln
81 65 70 75 80
83 Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys
84 85 90 95
86 Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr
87 100 105 110
89 Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu
90 115 120 125
92 Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
93 130 135 140
95 Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
96 145 150 155 160
98 Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
99 165 170 175
101 Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
102 180 185 190
104 Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
105 195 200 205
107 Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
108 210 215 220
110 Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
111 225 230 235 240
113 Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
114 245 250 255
116 Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
117 260 265 270
119 Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
120 275 280 285
122 Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
123 290 295 300
125 Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
126 305 310 315 320
128 Val Gln Ile
132 <210> SEQ ID NO: 3

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140 tgttttttga cagtaaatgt gtccttgatt atataattaac tagtcaaaga ggtgtttgta 180
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142 cagaaagcct ggatcagaaa accatcaccc taaaaaaaaca tgccttacat atttaacaca 300
143 ctctgaaatc cagtcaaaat atgactaaag gcccttgcca tgactgatgt attctcctgg 360
144 ccaacgccaa acaaatggga gccctggtac gagtgcgcct tcagggaact gtcacatttc 420
145 tacttggttt cttccttgtt attgtcataa taaaatgttt tctatgctgt ttagtgcaac 480
146 ttaggcccta ttctgtagaa gtctcctcta ctattcaggc cactcaaaaa ccccaaataa 540
147 ttgagttcaa aatcgacatc aagatataaa ggaatcagtg actaaatata tttcatatat 600
148 ggtattttta ttgattattg tgcgtgtctg acctagtatg gaggccttgg ctagaggctg 660
149 gtcagtttcc tctcttgagc agctgattaa atccacaccc caaccatttc ccttatcagg 720
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154 ttcagagctg ttttccacag aggtagttaa aagaactgga tttcaagtt cactttgcaa 1020
155 gagaanaaga aaactcagta gaagataatg gcaagtccag actggggata tgatgacaaa 1080
156 aatggtcctg aacaatggag caagctgtat cccattgcca atggaataa ccaatccct 1140
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169 tcaagaacac agccctgctt ctgacataat ccagttaaaa taataatttt taagaaataa 1920
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179 cttctcccca cgtttagcaag gacaatgctt ctctgccatt attacaacta gttagtttgc 2520
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183 tggagtatatag tgtgggtgttt tctgtttgttt tgtttgtttt ttgagacaag gtctcactct 2760
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188 <211> LENGTH: 261
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199 Asp Ile Lys Thr Ser Glu Thr Lys His Asp Thr Ser Leu Lys Pro Ile
200 35 40 45
202 Ser Val Ser Tyr Asn Pro Ala Thr Ala Lys Glu Ile Ile Asn Val Gly
203 50 55 60
205 His Ser Phe His Val Asn Phe Glu Asp Asn Asp Asn Arg Ser Val Leu
206 65 70 75 80
208 Lys Gly Gly Pro Phe Ser Asp Ser Tyr Arg Leu Phe Gln Phe His Phe
209 85 90 95
211 His Trp Gly Ser Thr Asn Glu His Gly Ser Glu His Thr Val Asp Gly
212 100 105 110
214 Val Lys Tyr Ser Ala Glu Leu His Val Ala His Trp Asn Ser Ala Lys
215 115 120 125
217 Tyr Ser Ser Leu Ala Glu Ala Ala Ser Lys Ala Asp Gly Leu Ala Val
218 130 135 140
220 Ile Gly Val Leu Met Lys Val Gly Glu Ala Asn Pro Lys Leu Gln Lys
221 145 150 155 160
223 Val Leu Asp Ala Leu Gln Ala Ile Lys Thr Lys Gly Lys Arg Ala Pro
224 165 170 175
226 Phe Thr Asn Phe Asp Pro Ser Thr Leu Leu Pro Ser Ser Leu Asp Phe
227 180 185 190
229 Trp Thr Tyr Pro Gly Ser Leu Thr His Pro Pro Leu Tyr Glu Ser Val
230 195 200 205
232 Thr Trp Ile Ile Cys Lys Glu Ser Ile Ser Val Ser Ser Glu Gln Leu
233 210 215 220
235 Ala Gln Phe Arg Ser Leu Leu Ser Asn Val Glu Gly Asp Asn Ala Val
236 225 230 235 240
238 Pro Met Gln His Asn Asn Arg Pro Thr Gln Pro Leu Lys Gly Arg Thr
239 245 250 255
241 Val Arg Ala Ser Phe
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246 <211> LENGTH: 18
247 <212> TYPE: PRT
248 <213> ORGANISM: Homo sapiens
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254 Gln Pro

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268   20           25
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274 <213> ORGANISM: Homo sapiens
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285 <211> LENGTH: 15
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <400> SEQUENCE: 8
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296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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320 <212> TYPE: DNA
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VERIFICATION SUMMARY

DATE: 03/27/2001

PATENT APPLICATION: US/09/802,674

TIME: 15:29:24

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date